

FIG. 1A

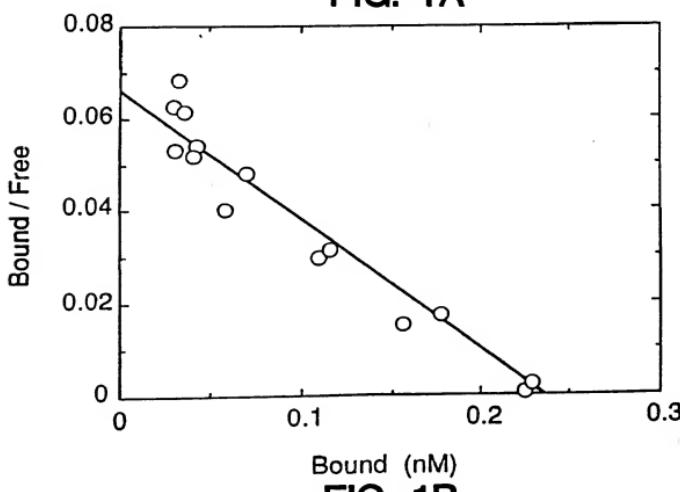


FIG. 1B

ATG TCA AAT ATT ACA GAT CCA CAG ATG TGG GAT TTT 86
 M t Ser Asn Ile Thr Asp Pro Gln Met Trp Asp Phe
 1 5 10
 GAT GAT CTA AAT TTC ACT GGC ATG CCA CCT GCA GAT GAA 125
 Asp Asp Leu Asn Phe Thr Gly Met Pro Pro Ala Asp Glu
 15 20 25
 GAT TAC AGC CCC TGT ATG CTA GAA ACT GAG ACA CTC AAC 164
 Asp Tyr Ser Pro Cys Met Leu Glu Thr Leu Asn
 30 35
 AAG TAT GTT GTG ATC ATC GCC TAT GCC CTA CTG TTC CTG 203
 Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu Val Phe Leu
 40 45 50
 CTG AGC CTG CTG GGA AAC TCC CTG GTG ATG CTG GTC ATC 242
 Leu Ser Leu Leu Gly Asn Ser Leu Val Met Leu Val Ile
 55 60
 TTA TAC AGC AGG GTC GGC CGC TCC GTC ACT GAT GTC TAC 281
 Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val Tyr
 65 70 75
 CTG CTG AAC CTG GCC TTG GCC GAC CTA CTC TTT GCC CTG 320
 Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu
 80 85 90
 ACC TTG CCC ATC TGG GCC GCC TCC AAG GTG AAT GGC TGG 359
 Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp
 95 100
 ATT TTT GGC ACA TTC CTG TGC AAG GTG GTC TCA CTC CTG 398
 Ile Phe Gly Thr Phe Leu Cys Lys Val Val Ser Leu Leu
 105 110 115
 AAG GAA GTC AAC TTC TAC AGT GGC ATC CTG CTG TTG GCC 437
 Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu Leu Ala
 120 125
 TGC ATC AGT GTG GAC CGT TAC CTG GCC ATT GTC CAT GCC 476
 Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val His Ala
 130 135 140
 ACA CGC ACA CTG ACC CAG AAG CGT CAC TTG GTC AAG TTT 515
 Thr Arg Thr Leu Thr Gln Lys Arg His Leu Val Lys Phe
 145 150 155
 GTT TGT CTT GGC TGC TGG GGA CTG TCT ATG AAT CTG TCC 554
 Val Cys Leu Gly Cys Trp Gly Leu Ser Met Asn Leu Ser
 160 165
 CTG CCC TTC CTT TTC CGC CAG GCT TAC CAT CCA AAC 593
 Leu Pro Phe Leu Phe Arg Gln Ala Tyr His Pro Asn
 170 175 180
 AAT TCC AGT CCA GTT TGC TAT GAG GTC CTG GGA AAT GAC 632
 Asn S r Ser Pro Val Cys Tyr Glu Val Leu Gly Asn Asp
 185 190
 ACA GCA AAA TGG CGG ATG GTG TTG CGG ATC CTG CCT CAC 671
 Thr Ala Lys Trp Arg Met Val Leu Arg Ile Leu Pro His
 195 200 205

FIG. 2A

ACC TTT GGC TTC ATC GTG CCG CTG TTT GTC ATG CTG TTC 710
 Thr Phe Gly Phe Ile Val Pro Leu Phe Val M t L u Phe
 210 215 220
 TGC TAT GGA TTC ACC CTG CGT ACA CTG TTT AAG GCC CAC 749
 Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His
 225 230 235
 ATG GGG CAG AAG CAC CGA GCC ATG AGG GTC ATC TTT GCT 788
 Met Gly Gln Lys His Arg Ala Met Arg Val Ile Phe Ala
 235 240 245
 GTC GTC CTC ATC TTC CTG CTT TGC TGG CTG CCC TAC AAC 827
 Val Val Leu Ile Phe Leu Leu Cys Trp Leu Pro Tyr Asn
 250 255
 CTG GTC CTG CTG GCA GAC ACC CTC ATG AGG ACC CAG GTG 866
 Leu Val Leu Leu Ala Asp Thr Leu Met Arg Thr Gln Val
 260 265 270
 ATC CAG GAG ACC TGT GAG CGC CGC AAC AAC ATC GGC CGG 905
 Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg
 275 280 285
 GCC CTG GAT GCC ACT GAG ATT CTG GGA TTT CTC CAT AGC 944
 Ala Leu Asp Ala Thr Glu Ile Leu Gly Phe Leu His Ser
 290 295
 TGC CTC AAC CCC ATC ATC TAC GCC TTC ATC GGC CAA AAT 983
 Cys Leu Asn Pro Ile Ile Tyr Ala Phe Ile Gly Gln Asn
 300 305 310
 TTT CGC CAT GGA TTC CTC AAG ATC CTG GCT ATG CAT GGC 1022
 Phe Arg His Gly Phe Leu Lys Ile Leu Ala Met His Gly
 315 320
 CTG GTC AGC AAG GAG TTC TTG GCA CGT CAT CGT GTT ACC 1061
 Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val Thr
 325 330 335
 TCC TAC ACT TCT TCG TCT GTC AAT GTC TCT TCC AAC CTC 1100
 Ser Tyr Thr Ser Ser Ser Val Asn Val Ser Ser Asn Leu
 340 345 350
 TGAAAACCAT CGATGAAGGA ATATCTCTTC TCAGAAGGAA AGAATAACCA 1150
 ACACCCCTGAG GTTGTGTGTG GAAGGTGATC TGGCTCTGGA CAGGCACTAT 1200
 CTGGGTTTTG GGGGGACGCT ATAGGATGTG GGGAAAGTTAG GAACTGGTGT 1250
 CTTCAGGGGC CACACCAACC TTCTGAGGAG CTGTTGAGGT ACCTCCAAGG 1300
 ACCGGCCTTT GCACCTCCAT GGAAACGAAG CACCATCATT CCCGTTGAAC 1350
 GTCACATCTT TAACCCACTA ACTGGCTAAT TAGCATGGCC ACATCTGAGC 1400
 CCCGAATCTG ACATTAGATG AGAGAACAGG GCTGAAGCTG TGTCTCATG 1450

FIG. 2B

AGGGCTGGAT GCTCTCGTTG ACCCTCACAG GAGCATCTCC TCAACTCTGA 1500
GTGTTAACG TTGAGCCACC AAGCTGGTGG CTCTGTGTGC TCTGATCCGA 1550
GCTCAGGGGG GTGGTTTCC CATCTCAGGT GTGTTGCAGT GTCTGCTGGA 1600
GACATTGAGG CAGGCAC TGC CAAACATCA ACCTGCCAGC TGGCCTTGTG 1650
AGGAGCTGGA AACACATGTT CCCCTTGGGG GTGGTGGATG AACAAAGAGA 1700
AAGAGGGTTT GGAAGCCAGA TCTATGCCAC AAGAACCCCC TTTACCCCCA 1750
TGACCAACAT CGCAGACACA TGTGCTGGCC ACCTGCTGAG CCCCAAGTGG 1800
AACGAGACAA GCAGCCCTTA GCCCTTCCCC TCTGCAGCTT CCAGGCTGGC 1850
GTGCAGCATC AGCATCCCTA GAAAGCCATG TGCAGCCACC AGTCCATTGG 1900
GCAGGCAGAT GTTCCTAATA AAGCTTCTGT TCC 1933

FIG. 2C

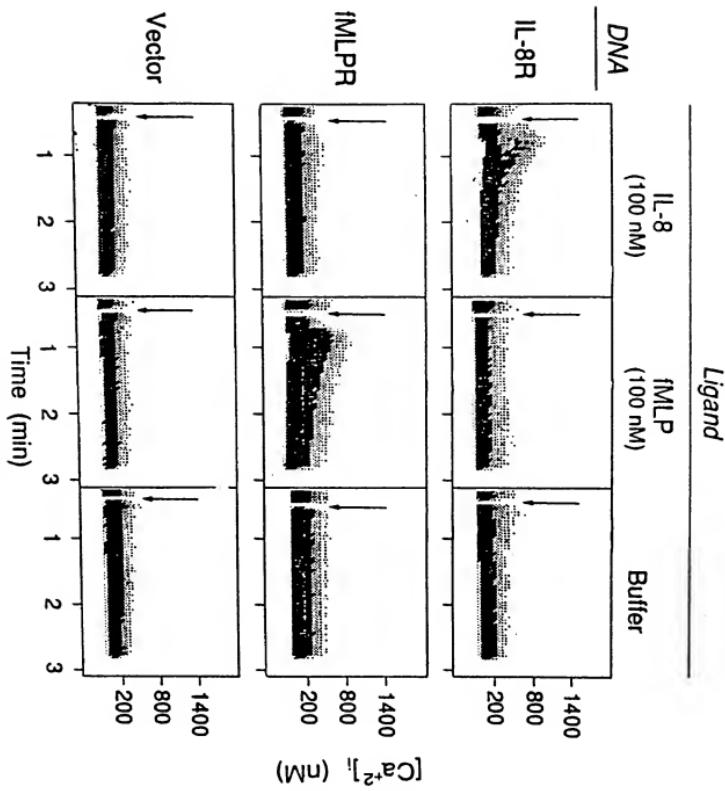


FIG. 3A

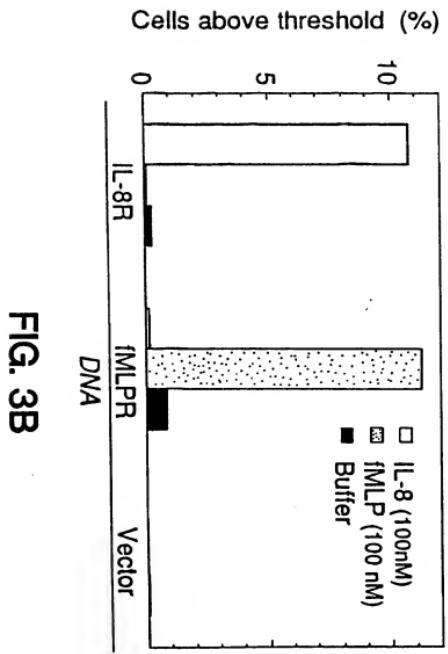


FIG. 3B

GAATTCAGT GTGCTGGCG CGCGGCCAA AGTGACCCG AGGGCCCTGAG 50
 TGCTCCAGTA GCCACCGCAT CTGGAGAAC ACCGGTTTAC ATG GAG 96
 Met Glu
 1
 Gly ATC AGT ATA TAC ACT TCA GAT AAC TAC ACC GAG GAA 135
 Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu
 5 10 15
 ATG GGC TCA GGG GAC TAT GAC TCC ATG AAG GAA CCC TGT 174
 Met Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys
 20 25
 TTC CGT GAA GAA AAT GCT AAT TTC AAT AAA ATC TTC CTG 213
 Phe Arg Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu
 30 35 40
 CCC ACC ATC TAC TCC ATC ATC TTC TTA ACT GGC ATT GTG 252
 Pro Thr Ile Tyr Ser Ile Ile Phe Leu Thr Gly Ile Val
 45 50
 GGC AAT GGA TTG GTC ATC CTG GTC ATG GGT TAC CAG AAG 291
 Gly Asn Gly Leu Val Ile Leu Val Met Gly Tyr Gln Lys
 55 60 65
 AAA CTG AGA AGC ATG ACG GAC AAG TAC AGG CTG CAC CTG 330
 Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
 70 75 80
 TCA GTG GCC GAC CTC CTC TTT GTC ATC ACG CTT CCC TTC 369
 Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe
 85 90
 TGG GCA GTT GAT GCC GTG GCA AAC TGG TAC TTT GGG AAC 408
 Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn
 95 100 105
 TCT CTA TGC AAG GCA GTC CAT GTC ATC TAC ACA GTC AAC 447
 Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn
 110 115
 CTC TAC AGC AGT GTC CTC ATC CTG GCC TTC ATC ACT CTG 486
 Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu
 120 125 130
 GAC CGC TAC CTG GCC ATC GTC CAC GCC ACC AAC ACT CAG 525
 Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln
 135 140 145
 AGG CCA AGG AAG CTG TTG GCT GAA AAG GTG GTC TAT GTT 564
 Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val
 150 155
 GGC GTC TGG ATC CCT GCC CTC CTG CTG ACT ATT CCC GAC 603
 Gly Val Trp Ile Pro Ala Leu Leu Thr Ile Pro Asp
 160 165 170
 TTC ATC TTT GCC AAC GTC AGT GAG GCA GAT GAC AGA TAT 642
 Phe Ile Phe Ala Asn Val Ser Glu Ala Asp Asp Arg Tyr
 175 180

FIG. 4A

ATC TGT GAC CGC TTC TAC CCC AAT GAC TTG TGG GTG GTT 681
 Ile Cys Asp Arg Ph Tyr Pro Asn Asp Leu Trp Val Val
 185 190 195
 GTG TTC CAG TTT CAG CAC ATC ATG GTT GGC CTT ATC CTG 720
 Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu
 200 205 210
 CCT GGT ATT GTC ATC CTG TCC TGC TAT TGC ATT ATC ATC 759
 Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile
 215 220 225
 TCC AAG CTG TCA CAC TCC AAG GGC CAC CAG AAG CGC AAG 798
 Ser Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys
 225 230 235
 GCC CTC AAG ACC ACA GTC ATC CTC ATC CTG GCT TTC 837
 Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe Phe
 240 245
 GCC TGT TGG CTG CCT TAC TAC ATT GGG ATC AGC ATC GAC 876
 Ala Cys Trp Leu Pro Tyr Tyr Ile Gly Ile Ser Ile Asp
 250 255 260
 TCC TTC ATC CTC CTG GAA ATC ATC AAG CAA GGG TGT GAG 915
 Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln Gly Cys Glu
 265 270 275
 TTT GAG AAC ACT GTG CAC AAG TGG ATT TCC ATC ACC GAG 954
 Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
 280
 285
 GCC CTA GCT TTC TTC CAC TGT TGT CTG AAC CCC ATC CTC 993
 Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu
 290 295 300
 TAT GCT TTC CTT GGA GCC AAA TTT AAA ACC TCT GCC CAG 1032
 Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln
 305 310
 CAC GCA CTC ACC TCT GTG AGC AGA GGG TCC AGC CTC AAG 1071
 His Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys
 315 320 325
 ATC CTC TCC AAA GGA AAG CGA GGT GGA CAT TCA TCT GTT 1110
 Ile Leu Ser Lys Gly Lys Arg Gly Gly His Ser Ser Val
 330 335 340 345
 TCC ACT GAG TCT GAG TCT TCA AGT TTT CAC TCC AGC TAAC 1150
 Ser Thr Glu Ser Ser Ser Phe His Ser Ser
 345 350 352
 ACAGATGTAA AAGACTTTTT TTTATACGAT AAATAACTTT TTTTTAAGTT 1200
 ACACATTTTT CAGATATAAA AGACTGACCA ATATTGTACA GTTTTTATTG 1250
 CTTGTTGGAT TTTTGTCTTG TGTTTCTTA GTTTTGTGA AGTTTAATTG 1300
 ACTTATTTAT ATAAATTTTT TTTGTTTCAT ATTGATGTGT GTCTAGGCAG 1350

FIG. 4B

GACCTGTGGC CAAGTTCTTA GTTGCTGTAT GTCTCGTGGT AGGACTGTAG 1400
AAAAGGGAAC TGAACATTCC AGAGCGTGTGTA GTGAATCACG TAAAGCTAGA 1450
AATGATCCCC AGCTGTTTAT GCATAGATAA TCTCTCCATT CCCGTGGAAC 1500
GTTTTCCCTG TTCTTAAGAC GTGATTTGC TGTAGAAGAT GGCACTTATA 1550
ACCAAAAGCCC AAAGTGGTAT AGAAATGCTG GTTTTCAGT TTTCAGGAGT 1600
GGGTTGATTT CAGCACCTAC AGTGTACAGT CTTGTATTAA GTTGTAAATA 1650
AAAGTACATG TTAAACTTAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1700
AAAAAAAAAA AAAGCGGCCG CCAGCACACT GGAATTC 1737

FIG. 4C

GAATTCCAGT GTGCTGGCGG CCGCCCCAGTG TGCTGGCGGC GGCAGTTGAG 50
 GGAAAGGACA GAGGTATGA GTGCCGTCAA GAGTGGCAGC CTGGAGTAGA 100
 GAAAACACTA AAGGTGGAGT CAAAAGACCT GAGTTCAAGT CCCAGCTCTG 150
 CCACTGGTTA GCTGTGGGAT CTCGAAAAG ACCCAGTGAA AAAAAAAA 200
 AAAGTGATGA GTTGTGAGGC AGGTGGCGGC CCTACTGCCT CAGGAGACCA 250
 TCGCAGCTC ATTTGCTTAA ATTTGCTGCT GACGGCTGCC ACCTCTCTAG 300
 AGGCACCTGG CGGGGAGCCT CTCAACATAA GACAGTGACC AGTCTGGTGA 350

| | | | | | | | | | | |
|------------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTCACAGCGG | GCACAGCC | ATG | AAC | TAC | CCG | CTA | ACG | CTG | GAA | 392 |
| | | Met | | Tyr | Pro | Leu | Thr | Leu | Glu | |
| | | 1 | | | | | | 5 | | |

ATG GAC CTC GAG AAC CTG GAG GAC CTG TTC TGG GAA CTG 431
 Met Asp Leu Glu Asn Leu Glu Asp Leu Phe Trp Glu Leu
 10 15 20

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAC | AGA | TTG | GAC | AAC | TAT | AAC | GAC | ACC | TCC | CTG | GTG | GAA | 470 |
| Asp | Arg | Leu | Asp | Asn | Tyr | Asn | Asp | Thr | Ser | Leu | Val | Glu | |
| 25 | | | | | | | | 30 | | | | | |

AAT CAT CTC TGC CCT GCC ACA GAG GGG CCC CTC ATG GCC 509
 Asn His Leu Cys Pro Ala Thr Glu Gly Pro Leu Met Ala
 35 40 45

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| TCC | TTC | AAG | GCC | GTG | TTC | GTG | CCC | GTG | GCC | TAC | AGC | CTC | 548 |
| Ser | Phe | Lys | Ala | Val | Phe | Val | Pro | Val | Ala | Tyr | Ser | Leu | |
| 50 | | | | | | | 55 | | | | 60 | | |

ATC TTC CTC CTG GGC GTG ATC GGC AAC GTC CTG GTG CTG 587
 Ile Phe Leu Leu Gly Val Ile Gly Asn Val Leu Val Leu
 65 70

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTG | ATC | CTG | GAG | CGG | CAC | CGG | CAG | ACA | CGC | AGT | TCC | ACG | 626 |
| Val | Ile | Leu | Glu | Arg | His | Arg | Gln | Thr | Arg | Ser | Ser | Thr | |
| 75 | | | | | | 80 | | | | | 85 | | |

GAG ACC TTC CTG TTC CAC CTG GCC GTG GCC GAC CTC CTG 665
 Glu Thr Phe Leu Phe His Leu Ala Val Ala Asp Leu Leu
 90 95

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CTG | GTC | TTC | ATC | TTG | CCC | TTT | GCC | GTG | GCC | GAG | GGC | TCT | 704 |
| Leu | Val | Phe | Ile | Leu | Pro | Phe | Ala | Val | Ala | Glu | Gly | Ser | |
| 100 | | | | | 105 | | | | | 110 | | | |

GTG GGC TGG GTC CTG GGG ACC TTC CTC TGC AAA ACT GTG 743
 Val Gly Trp Val Leu Gly Thr Phe Leu Cys Lys Thr Val
 115 120 125

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATT | GCC | CTG | CAC | AAA | GTC | AAC | TTC | TAC | TGC | AGC | AGC | CTG | 782 |
| Ile | Ala | Leu | His | Lys | Val | Asn | Phe | Tyr | Cys | Ser | Ser | Leu | |
| 130 | | | | | | | | | 135 | | | | |

FIG. 5A

CTC CTG GCC TGC ATC GCC GTG GAC CGC TAC CTG GCC ATT 821
 Leu Leu Ala Cys Ile Ala Val Asp Arg Tyr Leu Ala Ile
 140 145 150
 GTC CAC GCC GTC CAT GCC TAC CGC CAC CGC CGC CTC CTC 860
 Val His Ala Val His Ala Tyr Arg His Arg Arg Leu Leu
 155 160 165
 TCC ATC CAC ATC ACC TGT GGG ACC ATC TGG CTG GTG GGC 899
 Ser Ile His Ile Thr Cys Gly Thr Ile Trp Leu Val Gly
 165 170 175
 TTC CTC CTT GCC TTG CCA GAG ATT CTC TTC GCC AAA GTC 938
 Phe Leu Leu Ala Leu Pro Glu Ile Leu Phe Ala Lys Val
 180 185 190
 AGC CAA GGC CAT CAC AAC AAC TCC CTG CCA CGT TGC ACC 977
 Ser Gln Gly His His Asn Asn Ser Leu Pro Arg Cys Thr
 195 200 205
 TTC TCC CAA GAG AAC CAA GCA GAA ACG CAT GCC TGG TTC 1016
 Phe Ser Gln Glu Asn Gln Ala Glu Thr His Ala Trp Phe
 205 210 215
 ACC TCC CGA TTC CTC TAC CAT GTG GCG GGA TTC CTG CTG 1055
 Thr Ser Arg Phe Leu Tyr His Val Ala Gly Phe Leu Leu
 220 225 230
 CCC ATG CTG GTG ATG GGC TGG TGC TAC GTG GGG GTA GTG 1094
 Pro Met Leu Val Met Gly Trp Cys Tyr Val Gly Val Val
 230 235 240
 CAC AGG TTG CGC CAG GCC CAG CGG CGC CCT CAG CGG CAG 1133
 His Arg Leu Arg Gln Ala Gln Arg Arg Pro Gln Arg Gln
 245 250 255
 AAG GCA GTC AGG GTG GCC ATC CTG GTG ACA AGC ATC TTC 1172
 Lys Ala Val Arg Val Ala Ile Leu Val Thr Ser Ile Phe
 260 265 270
 TTC CTC TGC TGG TCA CCC TAC CAC ATC GTC ATC TTC CTG 1211
 Phe Leu Cys Trp Ser Pro Tyr His Ile Val Ile Phe Leu
 270 275 280
 GAC ACC CTG GCG AGG CTG AAG GCC GTG GAC AAT ACC TGC 1250
 Asp Thr Leu Ala Arg Leu Lys Ala Val Asp Asn Thr Cys
 285 290 295
 AAG CTG AAT GGC TCT CTC CCC GTG GCC ATC ACC ATG TGT 1289
 Lys Leu Asn Gly Ser Leu Pro Val Ala Ile Thr Met Cys
 300 305 310
 GAG TTC CTG GGC CTG GCC CAC TGC TGC CTC AAC CCC ATG 1328
 Glu Phe Leu Gly Leu Ala His Cys Cys Leu Asn Pro Met
 310 315 320
 CTC TAC ACT TTC GCC GGC GTG AAG TTC CGC ACT GAC CTG 1367
 Leu Tyr Thr Ph Ala Gly Val Lys Phe Arg Ser Asp L u
 325 330 335
 TCG CGG CTC CTG ACG AAG CTG GGC TGT ACC GGC CCT GCC 1406
 Ser Arg Leu Leu Thr Lys Leu Gly Cys Thr Gly Pro Ala
 340 345 350

FIG. 5B

TCC CTG TGC CAG CTC TTC CCT AGC TGG CGC AGG AGC AGT 1445
Ser Leu Cys Gln Leu Phe Pro Ser Trp Arg Arg Ser Ser
350 355

CTC TCT GAG TCA GAG AAT GCC ACC TCT CTC ACC ACG TTC TA 1486
Leu Ser Glu Ser Glu Asn Ala Thr Ser Leu Thr Thr Phe
360 365 370 372

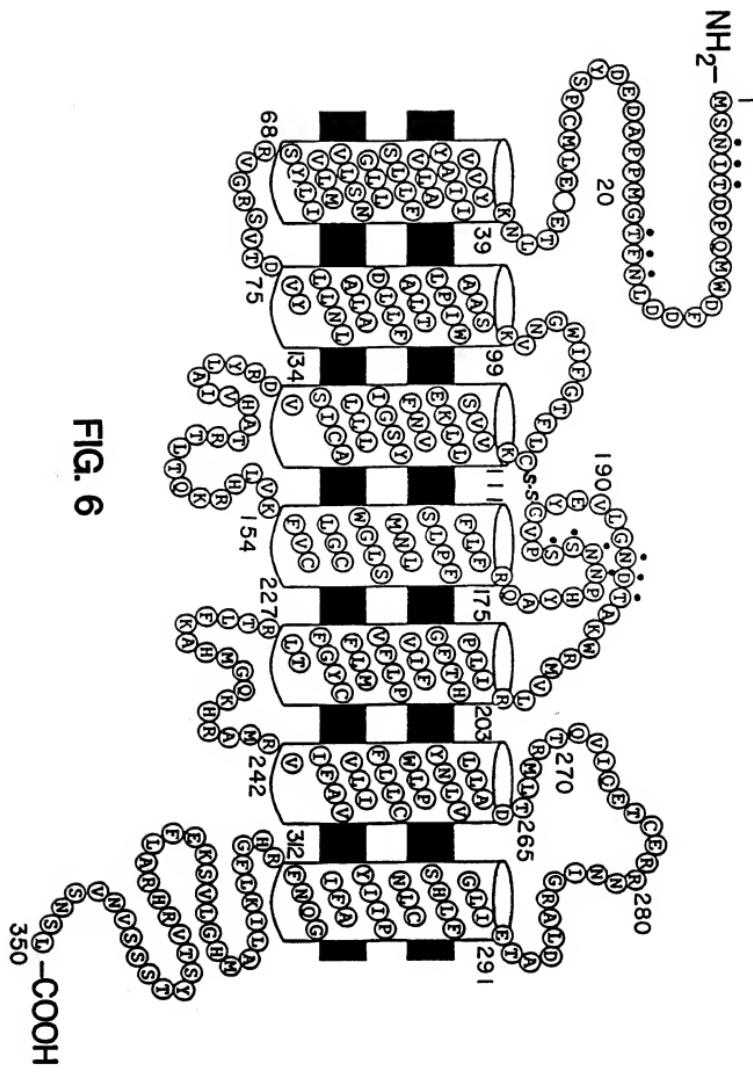
GGTC CCAGTGTCCC CTTTATTGC TGCTTTCCCT TGGGGCAGGC 1530

AGTGATGCTG GATGCTCCTT CCAACAGGAG CTGGGATCCT AAGGGCTCAC 1580

CGTGGCTAAG AGTGTCTAG GAGTATCCTC ATTTGGGTA GCTAGAGGAA 1630

CCAACCCCCA TTTCTAGAAC ATCCCGCGGC CGCCAGCACA CTGGAATTC 1679

FIG. 5C



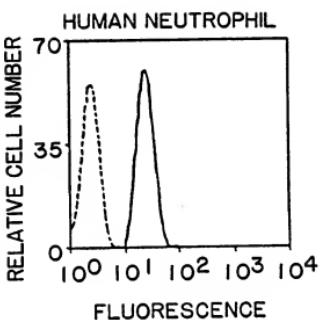


FIG. 7A

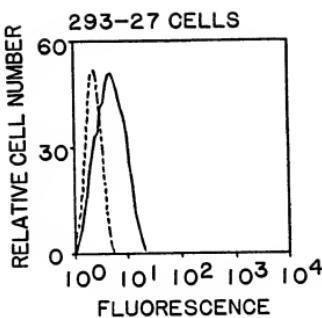


FIG. 7B

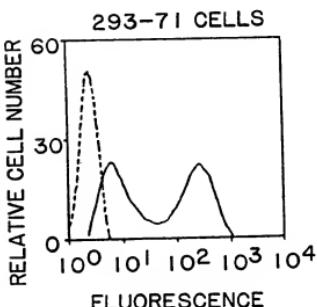


FIG. 7C

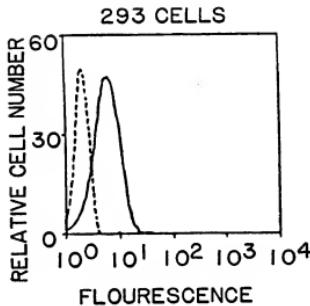


FIG. 7D

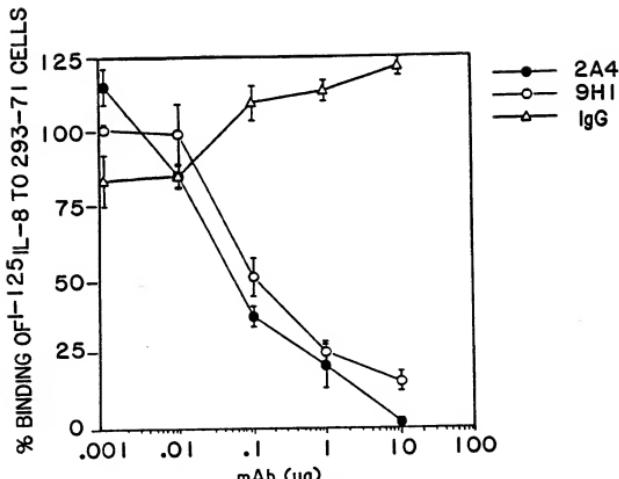


FIG. 8A

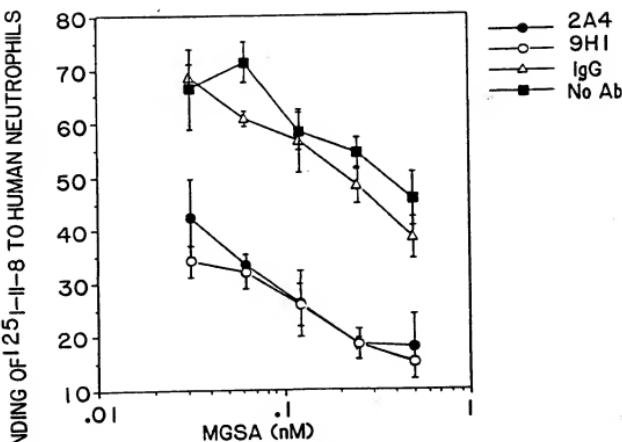


FIG. 8B

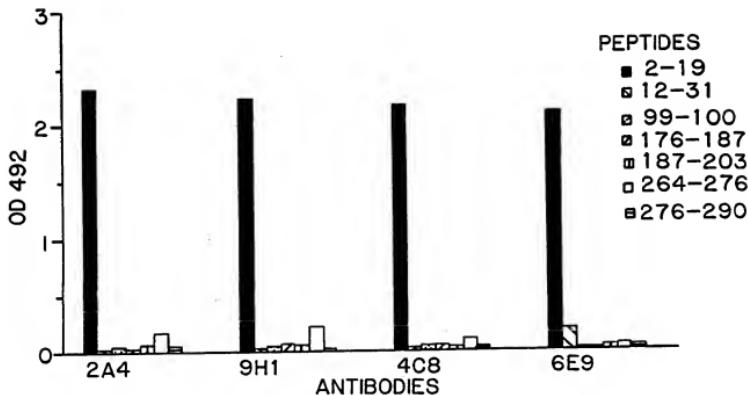


FIG. 9A

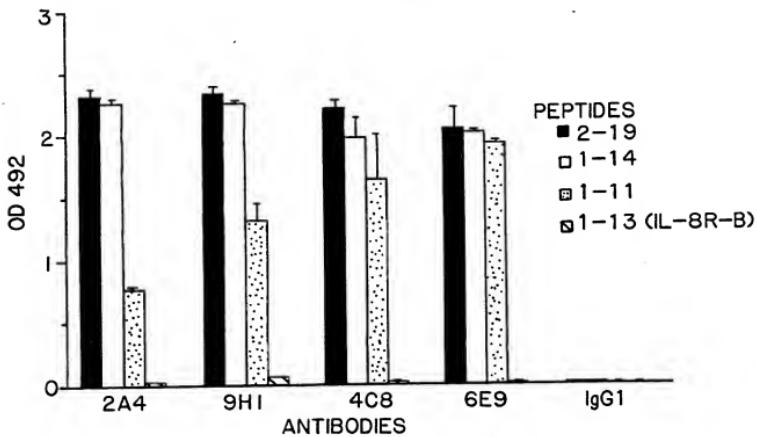


FIG. 9B

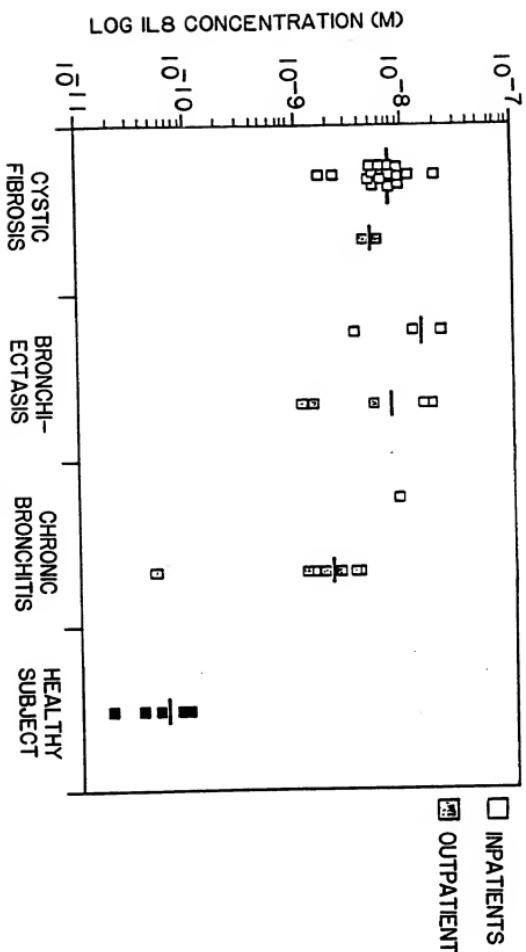


FIG. 10